

0590

11/06 OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/815,379

DATE: 09/06/2001
TIME: 10:42:08

Input Set : A:\1071635.app
Output Set: N:\CRF3\09062001\I815379.raw

3 <110> APPLICANT: RASTELLI, LUCA
4 GERRITSEN, MARY
6 <120> TITLE OF INVENTION: ANGIOGENESIS ASSOCIATED PROTEINS AND NUCLEIC ACIDS
7 ENCODING THE SAME
9 <130> FILE REFERENCE: 10716/35
11 <140> CURRENT APPLICATION NUMBER: 09/815,379
12 <141> CURRENT FILING DATE: 2001-03-22
14 <150> PRIOR APPLICATION NUMBER: 60/191,134
15 <151> PRIOR FILING DATE: 2000-03-22
17 <160> NUMBER OF SEQ ID NOS: 17
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2577
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1

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29 caattgcaga tttgagcaca atgtctgcag actgtgttga aaaactctga agaacctaat 180
30 taacacagga tgacctagga gtgattctaa gtctgtgtaa caagatatta ctcatagtg 240
31 aatgtgtcag tcttggtact gaatgctgca gataacagca agtaggttct cctttatttc 300
32 tgaagtattc acttgacctt ccatcagtaa gacggacttt tctaactctgt tcctggagat 360
33 attaatggaa tacagtcatg tccactcaag acgagaggca gatcaatact gaatatgctg 420
34 tgtcattgtt ggaacagttg aaactgtttt atgaacagca gttgtttact gacatagtgt 480
35 taattgttga gggcactgaa ttcccttgtc ataagatggt tcttgcaaca tgtagctctt 540
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39 atgtgttaca acgttgctga gaatatataa ttaaaaaaat aaatgcagag aattgtgtac 780
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41 tgggtggagca caagttcact gctgtgtatc atcaggacgc gttcatgcag ctgtcacatg 900
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47 cttcagaaaa tcctttagt ctttactctt ctgtctgtta cagcccccac gcagaaaaag 1260
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54 taccttgctg ttggcaatgg agtgcagcag ttgtggttca tgactgcatt tatgtgatga 1680
55 cactgaacct catgtactgt tattttccaa ggtctgactc atgggtagaa atggccatga 1740
56 gacagactag taggtccttt gcttcagctg cagcttttgg tgataaaatt ttctatattg 1800
57 gaggggttgc tattgctacc aattccggca taagactccc ctctggcact gtagatgggt 1860

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58 cttcagtaac tgtggaaatt tatgatgtga ataaaaatga gtggaaaatg gcagccaaca 1920
59 tccctgctaa gaggtactct gacccctgtg ttagagctgt tgtgatctca aattctctat 1980
60 gtgtgtttat gcgagaaacc cacttaaattg agcgagctaa atacgtcacc taccaatatg 2040
61 acctggaact tgaccggtgg tctctgcggc agcatatatc tgaacgtgta ctgtgggact 2100
62 tggggagaga ttttcgatgc actgtgggga aactctatcc atcctgcctt gaagagtctc 2160
63 catggaaacc accaacttat cttttttcaa cggatgggac agaagagttt gaactggatg 2220
64 gagaaatggg tgcactacca cctgtatagt ggggaagttc agggagtgcg cgcctgagtt 2280
65 atgtgctttg tcattttctt tgctaaacaa aagaggctat gaaagaacta aatatgagta 2340
66 cataaaattc tatctttgat aaattttatt tttatgccct acttaatat tgcatacagta 2400
67 taatatatat cagtgaagtct tacagaaaga tatgcttcca taatatgaaa tagattattc 2460
68 aataattgag aaactttatg tgtaatcatg agagtataag aatctggatt atctaacatt 2520
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73 <211> LENGTH: 623
74 <212> TYPE: PRT
75 <213> ORGANISM: Homo sapiens
77 <400> SEQUENCE: 2
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79 1 5- 10 15
81 Leu Leu Glu Gln Leu Lys Leu Phe Tyr Glu Gln Gln Leu Phe Thr Asp
82 20 25 30
84 Ile Val Leu Ile Val Glu Gly Thr Glu Phe Pro Cys His Lys Met Val
85 35 40 45
87 Leu Ala Thr Cys Ser Ser Tyr Phe Arg Ala Met Phe Met Ser Gly Leu
88 50 55 60
90 Ser Glu Ser Lys Gln Thr His Val His Leu Arg Asn Val Asp Ala Ala
91 65 70 75 80
93 Thr Leu Gln Ile Ile Ile Thr Tyr Ala Tyr Thr Gly Asn Leu Ala Met
94 85 90 95
96 Asn Asp Ser Thr Val Glu Gln Leu Tyr Glu Thr Ala Cys Phe Leu Gln
97 100 105 110
99 Val Glu Asp Val Leu Gln Arg Cys Arg Glu Tyr Leu Ile Lys Lys Ile
100 115 120 125
102 Asn Ala Glu Asn Cys Val Arg Leu Leu Ser Phe Ala Asp Leu Phe Ser
103 130 135 140
105 Cys Glu Glu Leu Lys Gln Ser Ala Lys Arg Met Val Glu His Lys Phe
106 145 150 155 160
108 Thr Ala Val Tyr His Gln Asp Ala Phe Met Gln Leu Ser His Asp Leu
109 165 170 175
111 Leu Ile Asp Ile Leu Ser Ser Asp Asn Leu Asn Val Glu Lys Glu Glu
112 180 185 190
114 Thr Val Arg Glu Ala Ala Met Leu Trp Leu Glu Tyr Asn Thr Glu Ser
115 195 200 205
117 Arg Ser Gln Tyr Leu Ser Ser Val Leu Ser Gln Ile Arg Ile Asp Ala
118 210 215 220
120 Leu Ser Glu Val Thr Gln Arg Ala Trp Phe Gln Gly Leu Pro Pro Asn
121 225 230 235 240
123 Asp Lys Ser Val Val Val Gln Gly Leu Tyr Lys Ser Met Pro Lys Phe
124 245 250 255

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126 Phe Lys Pro Arg Leu Gly Met Thr Lys Glu Glu Met Met Ile Phe Ile
127           260           265           270
129 Glu Ala Ser Ser Glu Asn Pro Cys Ser Leu Tyr Ser Ser Val Cys Tyr
130           275           280           285
132 Ser Pro Gln Ala Glu Lys Val Tyr Lys Leu Cys Ser Pro Pro Ala Asp
133           290           295           300
135 Leu His Lys Val Gly Thr Val Val Thr Pro Asp Asn Asp Ile Tyr Ile
136 305           310           315           320
138 Ala Gly Gly Gln Val Pro Leu Lys Asn Thr Lys Thr Asn His Ser Lys
139           325           330           335
141 Thr Ser Lys Leu Gln Thr Ala Phe Arg Thr Val Asn Cys Phe Tyr Trp
142           340           345           350
144 Phe Asp Ala Gln Gln Asn Thr Trp Phe Pro Lys Thr Pro Met Leu Phe
145           355           360           365
147 Val Arg Ile Lys Pro Ser Leu Val Cys Cys Glu Gly Tyr Ile Tyr Ala
148           370           375           380
150 Ile Gly Gly Asp Ser Val Gly Gly Glu Leu Asn Arg Arg Thr Val Glu
151 385           390           395           400
153 Arg Tyr Asp Thr Glu Lys Asp Glu Trp Thr Met Val Ser Pro Leu Pro
154           405           410           415
156 Cys Ala Trp Gln Trp Ser Ala Ala Val Val Val His Asp Cys Ile Tyr
157           420           425           430
159 Val Met Thr Leu Asn Leu Met Tyr Cys Tyr Phe Pro Arg Ser Asp Ser
160           435           440           445
162 Trp Val Glu Met Ala Met Arg Gln Thr Ser Arg Ser Phe Ala Ser Ala
163           450           455           460
165 Ala Ala Phe Gly Asp Lys Ile Phe Tyr Ile Gly Gly Leu His Ile Ala
166 465           470           475           480
168 Thr Asn Ser Gly Ile Arg Leu Pro Ser Gly Thr Val Asp Gly Ser Ser
169           485           490           495
171 Val Thr Val Glu Ile Tyr Asp Val Asn Lys Asn Glu Trp Lys Met Ala
172           500           505           510
174 Ala Asn Ile Pro Ala Lys Arg Tyr Ser Asp Pro Cys Val Arg Ala Val
175           515           520           525
177 Val Ile Ser Asn Ser Leu Cys Val Phe Met Arg Glu Thr His Leu Asn
178           530           535           540
180 Glu Arg Ala Lys Tyr Val Thr Tyr Gln Tyr Asp Leu Glu Leu Asp Arg
181 545           550           555           560
183 Trp Ser Leu Arg Gln His Ile Ser Glu Arg Val Leu Trp Asp Leu Gly
184           565           570           575
186 Arg Asp Phe Arg Cys Thr Val Gly Lys Leu Tyr Pro Ser Cys Leu Glu
187           580           585           590
189 Glu Ser Pro Trp Lys Pro Pro Thr Tyr Leu Phe Ser Thr Asp Gly Thr
190           595           600           605
192 Glu Glu Phe Glu Leu Asp Gly Glu Met Val Ala Leu Pro Pro Val
193           610           615           620
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1749
198 <212> TYPE: DNA

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199 <213> ORGANISM: Homo sapiens

201 <400> SEQUENCE: 3

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204 aacagaggag ggaaggcgtc ttaggactgc ctggatccag agcactttcc tcggcctcta 180
205 caggcctgtg tcgctatggg ttcccccgcc gccccggagg gagcgctggg ctacgtccgc 240
206 gagttcactc gccactcctc cgacgtgctg ggcaacctca acgagctgcg cctgcgcggg 300
207 atcctcactg acgtcacgct gctggttggc gggcaacccc tcagagcaca caaggcagtt 360
208 ctcatcgccct gcagtggctt ctctatttca atttccggg gccgtgcggg agtcggggtg 420
209 gacgtgctct ctctgcccgg gggtcgccaa gcgagaggct tcgcccctct attggacttc 480
210 atgtacactt cgcgcctgcg cctctctcca gccactgcac cagcagtcct agcggccgcc 540
211 acctatttgc agatggagca cgtggtccag gcatgccacc gttcatcca ggccagctat 600
212 gaacctctgg gcatctccct gcgccccctg gaagcagaac cccaacacc cccaacggcc 660
213 cctccaccag gtagtcccag gcgctccgaa ggacacccag acccacctac tgaatctcga 720
214 agctgcagtc aaggcccccc cagtccagcc agccttgacc ccaaggcctg caactggaaa 780
215 aagtacaagt acatcgctgt aaactctcag gcctcccaag caggagcctt ggtcggggag 840
216 agaagttctg gtcaaccttg cccccaagcc aggtcccca gtggagacga ggcctccagc 900
217 agcagcagca gcagcagcag cagcagcagt gaagaaggac ccattcctgg tcccagagc 960
218 aggtctcttc caactgctgc cactgtgcag ttcaaagtgt gggctccagc cagtaccccc 1020
219 tacctcctca catcccaggc tcaagacacc tctggatcac cctctgaacg ggctcgtcca 1080
220 ctacccggga gtgaattttt cagctgccag aactgtgagg ctgtggcagg gtgctcatcg 1140
221 gggctggact ccttggttcc tggggacgaa gacaaacctt ataagtgtca gctgtgccgg 1200
222 tcttcgttcc gctacaaggg caaccttgcc agtcaccgta cagtgcacac aggggaaaag 1260
223 ccttaacctt gctcaatctg cggagcccgt tttaacggc cagcaaacct gaaaacgcac 1320
224 agccgcatcc attcgggaga gaagccgtat aagtgtgaga cgtgcggctc gcgctttgta 1380
225 caggtaacga gccagcctcc aagtggcttc caaggcaaac ctgcaagagg tggggagggc 1440
226 caaaagggag ggttctgttc ctcccagagg caggacttga agtctcctcc ctcccaggtg 1500
227 gcacatctgc gggcgcacgt gctgatccac accggggaga agccctaccc ttgccctacc 1560
228 tgcggaaccc gcttcgcgca cctgcagacc ctcaagagcc acgttcgcat ccacaccgga 1620
229 gagaagcctt accactgcga cccctgtggc ctgcatttcc ggcacaagag tcaactgcgg 1680
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231 gggggggccc
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234 <210> SEQ ID NO: 4
235 <211> LENGTH: 518
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 4
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243 Phe Thr Arg His Ser Ser Asp Val Leu Gly Asn Leu Asn Glu Leu Arg
244 20 25 30
246 Leu Arg Gly Ile Leu Thr Asp Val Thr Leu Leu Val Gly Gly Gln Pro
247 35 40 45
249 Leu Arg Ala His Lys Ala Val Leu Ile Ala Cys Ser Gly Phe Phe Tyr
250 50 55 60
252 Ser Ile Phe Arg Gly Arg Ala Gly Val Gly Val Asp Val Leu Ser Leu
253 65 70 75 80
255 Pro Gly Gly Pro Glu Ala Arg Gly Phe Ala Pro Leu Leu Asp Phe Met
256 85 90 95

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258 Tyr Thr Ser Arg Leu Arg Leu Ser Pro Ala Thr Ala Pro Ala Val Leu
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261 Ala Ala Ala Thr Tyr Leu Gln Met Glu His Val Val Gln Ala Cys His
262           115           120           125
264 Arg Phe Ile Gln Ala Ser Tyr Glu Pro Leu Gly Ile Ser Leu Arg Pro
265           130           135           140
267 Leu Glu Ala Glu Pro Pro Thr Pro Thr Ala Pro Pro Pro Gly Ser
268 145           150           155           160
270 Pro Arg Arg Ser Glu Gly His Pro Asp Pro Pro Thr Glu Ser Arg Ser
271           165           170           175
273 Cys Ser Gln Gly Pro Pro Ser Pro Ala Ser Pro Asp Pro Lys Ala Cys
274           180           185           190
276 Asn Trp Lys Lys Tyr Lys Tyr Ile Val Leu Asn Ser Gln Ala Ser Gln
277           195           200           205
279 Ala Gly Ser Leu Val Gly Glu Arg Ser Ser Gly Gln Pro Cys Pro Gln
280           210           215           220
282 Ala Arg Leu Pro Ser Gly Asp Glu Ala Ser Ser Ser Ser Ser Ser
283 225           230           235           240
285 Ser Ser Ser Ser Ser Glu Glu Gly Pro Ile Pro Gly Pro Gln Ser Arg
286           245           250           255
288 Leu Ser Pro Thr Ala Ala Thr Val Gln Phe Lys Cys Gly Ala Pro Ala
289           260           265           270
291 Ser Thr Pro Tyr Leu Leu Thr Ser Gln Ala Gln Asp Thr Ser Gly Ser
292           275           280           285
294 Pro Ser Glu Arg Ala Arg Pro Leu Pro Gly Ser Glu Phe Phe Ser Cys
295           290           295           300
297 Gln Asn Cys Glu Ala Val Ala Gly Cys Ser Ser Gly Leu Asp Ser Leu
298 305           310           315           320
300 Val Pro Gly Asp Glu Asp Lys Pro Tyr Lys Cys Gln Leu Cys Arg Ser
301           325           330           335
303 Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Arg Thr Val His Thr
304           340           345           350
306 Gly Glu Lys Pro Tyr His Cys Ser Ile Cys Gly Ala Arg Phe Asn Arg
307           355           360           365
309 Pro Ala Asn Leu Lys Thr His Ser Arg Ile His Ser Gly Glu Lys Pro
310           370           375           380
312 Tyr Lys Cys Glu Thr Cys Gly Ser Arg Phe Val Gln Val Arg Ser Gln
313 385           390           395           400
315 Pro Pro Ser Gly Phe Gln Gly Lys Pro Ala Arg Gly Gly Val Gly Gln
316           405           410           415
318 Lys Gly Gly Phe Cys Ser Ser Gln Arg Gln Asp Leu Lys Ser Pro Pro
319           420           425           430
321 Ser Gln Val Ala His Leu Arg Ala His Val Leu Ile His Thr Gly Glu
322           435           440           445
324 Lys Pro Tyr Pro Cys Pro Thr Cys Gly Thr Arg Phe Arg His Leu Gln
325           450           455           460
327 Thr Leu Lys Ser His Val Arg Ile His Thr Gly Glu Lys Pro Tyr His
328 465           470           475           480
330 Cys Asp Pro Cys Gly Leu His Phe Arg His Lys Ser Gln Leu Arg Leu

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16